CLAIMS

1   1.   An apparatus comprising:

2   a sequence database configured to contain entries of sequences;

3   a sequence comparitor configured to receive a patient sample sequence, to

4   compare the patient sample sequence with entries in the sequence database

5   to determine closest matches, and to normalize a matching score of the

6   closest matches.

1   2.   The apparatus of claim A1, wherein the sequence comparitor is further

2   configured to determine whether the matching score of the closest matches

3   are within a confidence threshold.

1   3.   The apparatus of claim A2 further comprising:

2   a patient profile manager to reporting whether a sample patient identifier

3   associated with the patient sample sequence matches a matched patient

4   identifier associated with the closest match;

1   4.   The apparatus of claim A3 wherein the patient sample sequence is

2   sequenced from a virus.

1   5.   The apparatus of claim A4 wherein the virus is hepatitis or Human

2   Immunodeficiency Virus (HIV).

1   6.   The apparatus of claim A3 wherein the patient sample sequence is

2   sequenced from deoxyribonucleic acid (DNA).

1   7.   The apparatus of claim A5 wherein the confidence threshold is

2   approximately three standard deviations from an average normalized

3   score.

1   8.   A method comprising:

2   receiving a patient sample sequence, the patient sample sequence being associated

3   with a sample patient identifier;

4   comparing the patient sample sequence with entries in a sequence database to

5   determine closest matches, the closest matches being associated with a

6   matched patient identifier;

7   normalizing a matching score of the closest matches.

1   9.   The method of claim 8 further comprising:

2   determining whether the matching score of the closest matches are within a

3   confidence threshold.

1   10.   The method of claim 9 further comprising:

2   reporting the closest matches within the confidence threshold.

1   11.   The method of claim 9 further comprising:

2   reporting whether the sample patient identifier matches the matched patient

3   identifier;

1   12.   The method of claim 11 wherein the patient sample sequence is sequenced

2   from a virus.

1   13.   The method of claim 12 wherein the virus is hepatitis or Human

2   Immunodeficiency Virus (HIV).

1   14.   The method of claim 10 wherein the patient sample sequence is sequenced

2   from deoxyribonucleic acid (DNA).

1   15.   The method of claim 13 wherein the confidence threshold is approximately

2   three standard deviations from an average normalized score.

1   16.   A computer-readable medium encoded with data and instructions, the data

2   and instructions causing an apparatus executing the instructions to:

3   receive a patient sample sequence, the patient sample sequence being associated

4   with a sample patient identifier;

5   compare the patient sample sequence with entries in a sequence database to

6   determine closest matches, the closest matches being associated with a

7   matched patient identifier;

8   normalize a matching score of the closest matches.

1   17.   The computer-readable medium of claim 16 wherein the instruction further

2   causes an apparatus to:

3   determine whether the matching score of the closest matches are within a

4   confidence threshold.

1   18.   The computer-readable medium of claim 17 wherein the instruction further

2   causes an apparatus to:

3   report the closest matches within the confidence threshold.

1   19.   The computer-readable medium of claim 18 wherein the instruction further

2   causes an apparatus to:

3   report whether the sample patient identifier matches the matched patient identifier;

1   20.   The computer-readable medium of claim 19 wherein the patient sample

2   sequence is sequenced from a virus.

1   21.   The computer-readable medium of claim 20 wherein the virus is hepatitis

2   or Human Immunodeficiency Virus (HIV).

1   22.   The computer-readable medium of claim 18 wherein the patient sample

2   sequence is sequenced from deoxyribonucleic acid (DNA).

1   23.   The computer-readable medium of claim 21 wherein the confidence

2   threshold is approximately three standard deviations from an average

3   normalized score.

1   24.   An apparatus comprising:

2   means for receiving a patient sample sequence, the patient sample sequence being

3   associated with a sample patient identifier;

4   means for comparing the patient sample sequence with entries in a sequence

5   database to determine closest matches, the closest matches being

6   associated with a matched patient identifier;

7   means for normalizing a matching score of the closest matches.

1   25.   The apparatus of claim 24 further comprising:

2   means for determining whether the matching score of the closest matches are

3   within a confidence threshold.

1   26.   The apparatus of claim 25 further comprising:

2   means for reporting the closest matches within the confidence threshold.

1   27.   The apparatus of claim 26 further comprising:

2   means for reporting whether the sample patient identifier matches the matched

3   patient identifier;

1   28.   The apparatus of claim 27 wherein the patient sample sequence is

2   sequenced from a virus.

1   29.   The apparatus of claim 28 wherein the virus is hepatitis or Human

2   Immunodeficiency Virus (HIV).

1   30.   The apparatus of claim 26 wherein the patient sample sequence is

2   sequenced from deoxyribonucleic acid (DNA).

1   31.   The apparatus of claim 29 wherein the confidence threshold is

2   approximately three standard deviations from an average normalized

3   score.